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OM protein - protein search, using sw model

Run on: February 14, 2005, 02:44:53 ; Search time 29.9342 Seconds
(without alignments)
324.190 Million cell updates/sec

Title: US-09-757-415A-1_COPY_11_140
Perfect score: 696
Sequence: 1 DTVPNHRNKFVINDDG.....NNHQTELEVPRTPTPTTPG 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUTS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685	98.4	508	3	US-08-980-523-9
2	679	97.6	129	3	US-08-980-523-11
3	143.5	20.6	481	3	US-08-787-091-2
4	135	19.4	412	4	US-09-949-016-7584
5	134.5	19.3	145	4	US-09-270-767-57695
6	134.5	19.3	328	4	US-09-270-767-42405
7	79.5	11.4	412	4	US-09-949-016-11420
8	79	11.4	412	4	US-09-248-796A-20552
9	78	11.2	105	4	US-09-377-285B-5
10	78	11.2	1234	2	US-08-317-310A-15
11	78	11.2	1234	5	PCT-US95-13041-15
12	78	11.2	1242	4	US-09-508-691-1
13	78	11.2	1242	4	US-09-503-248-5
14	78	11.2	1242	4	US-09-903-199-5
15	78	11.2	1242	4	US-09-903-216-5
16	78	11.2	1242	4	US-09-903-063-5
17	78	11.2	1242	4	US-09-859-604-5
18	78	11.2	1243	2	US-08-557-139-2
19	77.5	11.1	112	3	US-08-980-523-10
20	77	11.1	38	3	US-08-787-091-9
21	76	10.9	505	4	US-09-270-767-41788
22	75	10.8	435	2	US-08-531-439B-4
23	74.5	10.7	709	4	US-09-489-847-132
24	72.5	10.4	153	4	US-09-270-767-32681
25	72.5	10.4	153	4	US-09-270-767-47898
26	72.5	10.4	541	3	US-09-134-001C-4497
27	68.5	9.8	342	4	US-09-543-681A-5131

28	68.5	9.8	1561	3	US-08-894-017-23	Sequence 23, Appl
29	68.5	9.8	1561	4	US-09-456-474-23	Sequence 23, Appl
30	68	9.8	159	4	US-09-508-691-5	Sequence 5, Appl
31	68	9.8	1321	2	US-08-317-310A-64	Sequence 64, Appl
32	67.5	9.7	118	3	US-08-936-165A-464	Sequence 464, Appl
33	67.5	9.7	342	4	US-09-489-039A-14092	Sequence 14092, A
34	67	9.6	144	4	US-09-134-000C-4435	Sequence 4435, Ap
35	67	9.6	233	4	US-09-710-279-784	Sequence 784, App
36	67	9.6	413	3	US-09-215-694-6	Sequence 6, Appl
37	67	9.6	492	3	US-09-134-001C-3895	Sequence 3895, Ap
38	66.5	9.6	1817	3	US-09-004-838-125	Sequence 125, App
39	66	9.5	378	3	US-09-134-001C-5487	Sequence 5487, Ap
40	66	9.5	441	4	US-09-270-767-47360	Sequence 47360, A
41	65.5	9.4	237	4	US-09-710-279-182	Sequence 182, App
42	65.5	9.4	380	4	US-09-710-279-1402	Sequence 1402, Ap
43	65.5	9.4	794	4	US-09-134-001C-4497	Sequence 4497, Ap
44	65.5	9.4	962	3	US-09-134-001C-4497	Sequence 4497, Ap
45	65	9.3	268	4	US-09-438-185A-1041	Sequence 1041, Ap

ALIGNMENTS

RESULT 1
US-08-980-523-9
; Sequence 9, Application US/08980523
; Patent No. 6310181
; GENERAL INFORMATION:
; APPLICANT: Kouhara, Haruhiko
; APPLICANT: Spivak-Kroizman, Taly
; APPLICANT: Lax, Irit
; APPLICANT: Schlesinger, Joseph
; TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980.523
; FILING DATE: December 1, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/21851
; FILING DATE: December 1, 1997
; APPLICATION NUMBER: 60/032.093
; FILING DATE: December 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 508 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-980-523-9

Query Match 98.4%; Score 685; DB 3; Length 508;
Best Local Similarity 97.7%; Pred. No. 6.3e-77;
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTVPDHNKFKVINVDGDELGSGIMELTDTLLYTRKRDSDVKWHYLCRLRRYGYDSN 60
Db 1 DTVPDHNKFKVINVDGDELGSGIMELTDTLLYTRKRDSDVKWHYLCRLRRYGYDSN 60

Qy 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELEVP 120
Db 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELEVP 120

Qy 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 2

US-08-980-523-11
; Sequence 11, Application US/08980523
; Patent No. 6310181
; GENERAL INFORMATION:
; APPLICANT: Kouhara, Haruhiko
; APPLICANT: Spivak-Kroizman, Taly
; APPLICANT: Lax, Irit
; APPLICANT: Schllessinger, Joseph
; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Fast-SEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: December 1, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/21851
; FILING DATE: December 1, 1997
; APPLICATION NUMBER: 60/032,093
; FILING DATE: December 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-523-11

Query Match 97.6%; Score 679; DB 3; Length 129;
Best Local Similarity 97.7%; Pred. No. 5.2e-77;

Matches 126; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTVPDHNKFKVINVDGDELGSGIMELTDTLLYTRKRDSDVKWHYLCRLRRYGYDSN 60
Db 1 DTVPDHNKFKVINVDGDELGSGIMELTDTLLYTRKRDSDVKWHYLCRLRRYGYDSN 60

Qy 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELEVP 120
Db 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELEVP 120

Qy 121 RTPRTPTTPG 129
Db 121 RTPRTPTTPG 129

RESULT 3

US-08-787-091-2
; Sequence 2, Application US/08787091
; Patent No. 6100386
; GENERAL INFORMATION:
; APPLICANT: Carpino, Nicholas A.
; APPLICANT: Kobayashi, Ryuji
; APPLICANT: Wisniewski, David G.
; APPLICANT: Strife, Annabel O'C.
; APPLICANT: Clarkson, Bayard D.
; TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in
; TITLE OF INVENTION: Chronic Myelogenous Leukemia
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,091
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,418
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-05pa
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 481 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-787-091-2

Query Match 20.6%; Score 143.5; DB 3; Length 481;
Best Local Similarity 29.5%; Pred. No. 3.7e-09;
Matches 33; Conservative 20; Mismatches 50; Indels 9; Gaps 2;

Qy 24 GSGIMELTDTLLYTRKRDSDVKWHYLCRLRRYGYDSNLFSPFSGRRRCOTGGQIF 77
Db 172 GSYVLRVEAERLTLLTVGAQSQILEPLLSWPYLLRRYGRDKVMFSEAGRCPSGPTF 231

Qy 78 AFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELEVPRTPTP 126
Db 232 TFOTAQGNDFQAVETAHROKAGQAGQGHVLRADSHSHEGVAEGKLPSPP 283

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RESULT 4
US-09-949-016-7584
; Sequence 7584, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7584
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7584

Query March 19.4%; Score 135; DB 4; Length 412;
Best Local Similarity 34.0%; Pred. No. 3.4e-08;
Matches 33; Conservative 13; Mismatches 33; Indels 18; Gaps 3;

Qy 47 WHYLCRLRYGYDSNLFSPESGRRCCTGGIAPKCARAEELFMQLQETM--QNNNSINVVE 104
Db 194 WPYEFLRFGDKVTFSEAGRCVSGSGNFEFTQGNIEIFLAEEAISAKNAAPATP 253
Qy 105 EPVVNNHQTLEVEPR-----TPTPTPT 129
Db 254 QP----QPATTPASIPRRDPSYSRPHDSLPPSPPTT 286

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RESULT 5
US-09-270-767-57695
; Sequence 57695, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57695
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57695

Query Match      19.3%; Score 134.5; DB 4; Length 145;
Best Local Similarity 24.8%; Pred. No. 9,1e-09;
Matches 31; Conservative 25; Mismatches 40; Indels 29; Gaps 3

Qy 27 IMELTDTLLIYTRKDS--VKWHYLCURRGYDSNLFSFSGRCQTGGIFAFKCARA 84
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 5  MLQMTPTQLQKSEDLGATIAWPPYRIRKYGKGTTFEAGRKCTTGEGVFTLLDHTNP 64
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 85 EELF-----NMLQEIIMONNSINVVE-----EPVVERNNHOTEL 117
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 65 QEVFRCSAKMKSMKLLISGDSLSLTLECGENQFSAAGACGECRSRSLPPSPSSNPHGGEF 124
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 118 EVPRIT 122
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 EINST 129
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 6
US-09-270-767-42405
; Sequence 42405, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42405
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42405

Query Match          19.3%   Score 134.5;   DB 4;   Length 328;
Best Local Similarity 24.8%;   Pred.No.2.9e-08;
Matches 31;   Conservative 25;   Mismatches 40;   Indels 29;   Gaps 3;

Qy 27 IMELTDELLIYTRKDS--VKHYHLCRLRRGYDSNLFSPESGRCQTGGQIFAFKCARA 84
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 188 MLQWTPTELQKSDLGATIAMVYRIRKYGYRDGKFTFAGRKCTTGEGVFTLDHTNP 247
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 85 BELP-----NMLQETMNNNSINVVE-----EPVVERNNHQTEL 117
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 248 QEVPRCMSAKMKSNNKLLISGDSLSTLCEGNQFSAAGMEPGSRSLPSPSSPHGGEF 307
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 118 EVPR 122
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 308 EINST 312
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 7
US-09-949-016-11420
; Sequence 11420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11420
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11420

Query Match          11.4%; Score 79.5; DB 4; Length 412;
Best Local Similarity 20.8%; Pred. No. 0.3;
Matches 27; Conservative 32; Mismatches 48; Indels 23; Gaps 6;

Qy      2  TVPDNHNKPKVINVDGNGELSGIMELT---DTELILYTRKRDSSVKWHY--LCLREYG 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      225  SIPQKRWNLVTIEND----TPLELSKYVDISIALTRNRTRRWYTCPLCGKQFN 279
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      57  YDSNLFSGFSGRRCCQTGGGIAFAFKCAAEELFNLQELMQNNSINVEEVP-----V 108
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      280  ESSYLIHQH---RTHTEK--PYDCNHCCKGSFNHKTNLNKRHTHTGKPKYSCQCGKNF 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



```

; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13041
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,310
; FILING DATE: 03-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-022PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-13041-15

Query Match 11.2%; Score 78; DB 5; Length 1234;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNNMLQIMQNNINNVVEEPPVVERN 111
DB 206 IRRCGHSENFIEVGRSAVTGPGEFWMQ-----VDDSVVAQN 243

QY 112 NHOATELEVR 121
DB 244 MHTILEAMR 253

RESULT 12
US-09-508-691-1
; Sequence 1, Application US/09508691
; Patent No. 6498139
; GENERAL INFORMATION:
; APPLICANT: YAZAKI, YOSHIO
; APPLICANT: ASANO, TOMOICHIRO
; APPLICANT: KUBO, HIDEO
; APPLICANT: KANDA, AKIRA
; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
; FILE REFERENCE: 4895-0019-OPCT
; CURRENT APPLICATION NUMBER: US/09/508,691
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/JP98/04293
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: JP9-263719
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-508-691-1
Query Match 11.2%; Score 78; DB 4; Length 1242;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNNMLQIMQNNINNVVEEPPVVERN 111
DB 211 IRRCGHSENFIEVGRSAVTGPGEFWMQ-----VDDSVVAQN 248

QY 112 NHOATELEVR 121
DB 249 MHTILEAMR 258

RESULT 13
US-09-903-248-5
; Sequence 5, Application US/09903248
; Patent No. 6783758
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV5
; CURRENT APPLICATION NUMBER: US/09/903,248
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match 11.2%; Score 78; DB 4; Length 1242;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNNMLQIMQNNINNVVEEPPVVERN 111
DB 211 IRRCGHSENFIEVGRSAVTGPGEFWMQ-----VDDSVVAQN 248

QY 112 NHOATELEVR 121
DB 249 MHTILEAMR 258

RESULT 14
US-09-903-199-5
; Sequence 5, Application US/09903199
; Patent No. 6797696
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV4
; CURRENT APPLICATION NUMBER: US/09/903,199
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 03:10:48 ; Search time 78.6842 Seconds
(without alignments)
539.846 Million cell updates/sec

Title: US-09-757-415a-1_COPY_11_140
Perfect score: 696
Sequence: 1 DTVPDHRNKKFVINVDDG.....NNHQTELEVPRTPTPTPG 130

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	100.0	508	10	US-09-757-415a-1
2	696	100.0	508	14	US-10-146-473-67
3	696	100.0	521	15	US-10-276-774-2192
4	685	98.4	508	9	US-09-731-660A-1
5	679	97.6	129	9	US-09-731-660A-3
6	143.5	20.6	541	13	US-10-001-870-179
7	141	20.3	359	9	US-09-789-913-58
8	137.5	19.8	331	15	US-10-307-928A-6
9	120.5	17.3	440	15	US-10-112-944-285
10	111.5	16.0	289	14	US-10-106-698-6260
11	95.5	13.7	268	14	US-10-029-386-33396
12	95.5	13.7	268	15	US-10-264-049-2340
13	78	11.2	105	14	US-10-192-081-5

14	78	11.2	114	9	US-09-731-660A-2	Sequence 2, Appli
15	78	11.2	1231	15	US-10-694-874-3	Sequence 3, Appli
16	78	11.2	1242	9	US-09-903-248-5	Sequence 5, Appli
17	78	11.2	1242	9	US-09-859-604-5	Sequence 5, Appli
18	78	11.2	1242	9	US-09-903-063-5	Sequence 5, Appli
19	78	11.2	1242	9	US-09-903-216-5	Sequence 5, Appli
20	78	11.2	1242	9	US-09-903-199-5	Sequence 5, Appli
21	78	11.2	1242	9	US-09-903-023-5	Sequence 5, Appli
22	78	11.2	1242	10	US-09-436-184-5	Sequence 5, Appli
23	78	11.2	1242	13	US-10-085-027-1	Sequence 1, Appli
24	78	11.2	1242	15	US-10-694-874-1	Sequence 1, Appli
25	78	11.2	1242	16	US-10-735-512-29	Sequence 29, Appli
26	78	11.2	1316	15	US-10-334-143-10	Sequence 10, Appli
27	75	10.8	99	15	US-10-424-599-217303	Sequence 217303
28	75	10.8	537	13	US-10-047-542-74	Sequence 74, Appli
29	74.5	10.7	520	15	US-10-282-122A-71887	Sequence 71887, A
30	74.5	10.7	523	16	US-10-437-963-124637	Sequence 124637, A
31	74.5	10.7	709	15	US-10-351-334-132	Sequence 132, App
32	74.5	10.7	973	15	US-10-276-774-2310	Sequence 2310, Ap
33	74	10.6	105	15	US-10-424-599-213391	Sequence 213391
34	74	10.6	428	15	US-10-282-122A-45402	Sequence 45402, A
35	73	10.5	169	16	US-10-767-701-52386	Sequence 52386, A
36	72.5	10.4	384	16	US-10-437-963-125379	Sequence 125379, A
37	72.5	10.4	437	14	US-10-156-761-12680	Sequence 12680, A
38	72.5	10.4	501	14	US-10-029-386-32319	Sequence 32319, A
39	72.5	10.4	519	15	US-10-282-122A-71027	Sequence 71027, A
40	72	10.3	530	15	US-10-094-749-2723	Sequence 2723, Ap
41	72	10.3	1331	14	US-10-087-464-50	Sequence 50, Appli
42	71.5	10.3	1309	15	US-10-369-493-1656	Sequence 1656, Ap
43	71	10.2	516	15	US-10-282-122A-47351	Sequence 47351, A
44	71	10.2	633	15	US-10-425-114-43531	Sequence 43531, A
45	70.5	10.1	749	9	US-09-899-569A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-757-415A-1
; Sequence 1, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757,415A
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-757-415A-1

Query Match	100.0%;	Score 696;	DB 10;	Length 508;
Best Local Similarity	100.0%;	Pred. No. 8.1e-71;		
Matches 130;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DTVPDHRNKKFVINVDDG	1	DTVPDHRNKKFVINVDDG
DB	11	DTVPDHRNKKFVINVDDG	11	DTVPDHRNKKFVINVDDG
QY	61	LFSFSGRCQGGI	61	LFSFSGRCQGGI
DB	71	LFSFSGRCQGGI	71	LFSFSGRCQGGI
QY	121	RTPTPTTPTG	121	RTPTPTTPTG
DB	131	RTPTPTTPTG	131	RTPTPTTPTG

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RESULT 2
US-10-146-473-67
; Sequence 67, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-67

Query Match      100.0%; Score 696; DB 14; Length 508;
Best Local Similarity 100.0%; Pred. No. 8.1e-71;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 3
US-10-276-774-2192
; Sequence 2192, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2192
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2192

Query Match      100.0%; Score 696; DB 15; Length 521;
Best Local Similarity 100.0%; Pred. No. 8.4e-71;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 24 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 83

QY 61 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

Query Match      98.4%; Score 685; DB 9; Length 508;
Best Local Similarity 97.7%; Pred. No. 1.5e-69;
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 4
US-09-731-660A-1
; Sequence 1, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, TALY
; APPLICANT: LAX, IRIT
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN FR52 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-660A-1

Query Match      98.4%; Score 685; DB 9; Length 508;
Best Local Similarity 97.7%; Pred. No. 1.5e-69;
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDDGSELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFSGRRRCCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 5
US-09-731-660A-3
; Sequence 3, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, TALY
; APPLICANT: LAX, IRIT
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN FR52 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 129
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-660A-3

Query Match
Best Local Similarity 97.6%; Score 679; DB 9; Length 129;
Matches 126; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPNHRNKFVINVDGNGELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
   |||||
Db 1 DTVPNHRNKFVINVDGNGELGSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
   |||||

QY 61 LFSFSGRCQCGGIFAFKARAELEFNMLQEIOMNNSINVVEBPVVERNHHQTELEVP 120
   |||||
Db 61 LFSFSGRCQCGGIFAFKARAELEFNMLQEIOMNNSINVVEBPVVERSSHQTELEVP 120
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QY 121 RTPRTPTTP 129
   |||||
Db 121 RTPRTPTTP 129
   |||||

RESULT 6
US-10-001-870-179
; Sequence 179, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 179
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-870-179

Query Match
Best Local Similarity 20.6%; Score 143.5; DB 13; Length 541;
Matches 33; Conservative 20; Mismatches 50; Indels 9; Gaps 2;

QY 24 GSGIMELTDTLLYTRKDS-----VKWHYLCRLRYGYDSNLFSESGRCQCGGIF 77
   |||||
Db 248 GSYLVRAERITLLTVGAQSQILEPLLSWPYTLRLRYGRDKVMFSEAGRCPSGPGTF 307
   |||||

QY 78 AFKARAELEFNMLQEIOMNNSINVVE---BPVVERNHHQTELEVPRTPTP 126
   |||||
Db 308 TPQTAGNDIFQAVETAIHRQAQKAGQGHVDLRADSHGEVAGKLPSP 359
   |||||

RESULT 7
US-09-789-919-58
; Sequence 58, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; APPLICANT: Moore, Kateri
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789,919
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 58
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; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-789-919-58

Query Match
Best Local Similarity 20.3%; Score 141; DB 9; Length 359;
Matches 36; Conservative 20; Mismatches 47; Indels 24; Gaps 3;

QY 23 LSGIMEITDTLLYTRKDSVKWHYLCRLRYGYDSNLFSESGRCQCGGIFAFKCA 82
   |||||
Db 184 LQDDIQLRET-----SKPQACFSWPYRFLRYGSDKGVSEAGRCDCSGLFAFSSP 238
   |||||

QY 83 RASELFNMLQEIOMNNSINVVE-----BPVVERNHHQTELEVPRTPTP 124
   |||||
Db 239 RAPDTCGVAAAIARQRERLPELAMPCCPLPRALSLPSLEPPGELREVAAPGFELETPRK 298
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QY 125 TP-TTPG 130
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Db 299 LPLTDPG 305
   |||||

RESULT 8
US-10-307-928A-6
; Sequence 6, Application US/10307928A
; Publication No. US20030229016A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Catterton, Elina
; APPLICANT: Edinger, Shalomit R.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Saasha)
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 24102-502D
; CURRENT APPLICATION NUMBER: US/10/307,928A
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,495
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/383,744
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/384,024
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/401,788
; PRIOR FILING DATE: 2002-08-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: CuraSeqList version 0.1
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; SEQ ID NO 6
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-928A-6

Query Match
Best Local Similarity 19.8%; Score 137.5; DB 15; Length 331;
Matches 34; Conservative 19; Mismatches 42; Indels 13; Gaps 3;

Qy 24 GSGIMELTDELILYTRKRDVSK---WHYLCRLRYGYDSNLFPSFSGRRRCQTGGIFAPK 80
Db 153 GECTMQITHENIYLDIHNNKXVLMWPLSSRLRYGRDSTWTFESGRMCDTGEGLFTQ 212

Qy 81 CARAEELFNLMQEIOMNNSINVVEE-----PVERNNHOTELEVPRT 122
Db 213 TREGE---MIYQKVHSATLIAEQHERLMLMEQKARLQTSLEPWT 256

RESULT 9
US-10-112-944-285
; Sequence 285, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_FL_Genes version 5.0
; SEQ ID NO 285
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-285

Query Match
Best Local Similarity 17.3%; Score 120.5; DB 15; Length 440;
Matches 35; Conservative 16; Mismatches 38; Indels 29; Gaps 5;

Qy 23 LGSGIMELTDE--LILYTRKRDVSKWHYLCRLRYGYDSNLFPSFSGRRRCQTGGIFAPK 80
Db 184 LGPDAIQLRAKGTQALYS-----WPYHFLRLKLGDKGVFSEAGRRCHSGEGLFAPS 236

; SEQ ID NO 81
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6260

Query Match
Best Local Similarity 16.0%; Score 111.5; DB 14; Length 289;
Matches 20; Conservative 15; Mismatches 26; Indels 3; Gaps 1;

Qy 28 MELTDELILYTRKRDVSK---WHYLCRLRYGYDSNLFPSFSGRRRCQTGGIFAPKCARA 84
Db 202 LQITHENIYLDIHNPVKLVSWKLCXXRYGRDATRTTFEAGRMCDAGEGLYTFQTQEG 261

Qy 85 BELF 88
Db 262 EQIY 265

RESULT 11
US-10-029-386-33396
; Sequence 33396, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33396
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006544.19

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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P56945, EVALUJE 2.00e-03
US-10-029-386-33396

Query Match      13.7%; Score 95.5; DB 14; Length 268;
Best Local Similarity 27.5%; Pred. No. 0.025;
Matches 19; Conservative 16; Mismatches 31; Indels 3; Gaps 1;

QY 61 LPSFSGRCQTGGIFAFKCAAEELFNNLQEIOMQNSINNVVE---EPVVERNHHQTEL 117
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Db 2 MFSFEAGRCPSGPGTFTTQAGNDIFQAVETAIHQKAGQKAGQGHDLVLRADSHGEV 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 EVPTPTPT 126
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 AEGKLPSP 70
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RESULT 12
US-10-264-049-2340
; Sequence 2340, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2340
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2340

Query Match      13.7%; Score 95.5; DB 15; Length 268;
Best Local Similarity 27.5%; Pred. No. 0.025;
Matches 19; Conservative 16; Mismatches 31; Indels 3; Gaps 1;

QY 61 LPSFSGRCQTGGIFAFKCAAEELFNNLQEIOMQNSINNVVE---EPVVERNHHQTEL 117
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Db 2 MFSFEAGRCPSGPGTFTTQAGNDIFQAVETAIHQKAGQKAGQGHDLVLRADSHGEV 61
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QY 118 EVPTPTPT 126
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 AEGKLPSP 70
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
US-10-192-381-5
; Sequence 5, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P56945, EVALUJE 2.00e-03
US-10-029-386-33396

Query Match      13.7%; Score 95.5; DB 14; Length 268;
Best Local Similarity 27.5%; Pred. No. 0.025;
Matches 19; Conservative 16; Mismatches 31; Indels 3; Gaps 1;

QY 61 LPSFSGRCQTGGIFAFKCAAEELFNNLQEIOMQNSINNVVE---EPVVERNHHQTEL 117
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2 MFSFEAGRCPSGPGTFTTQAGNDIFQAVETAIHQKAGQKAGQGHDLVLRADSHGEV 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 EVPTPTPT 126
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 AEGKLPSP 70
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-09-731-660A-2
; Sequence 2, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, Taly
; APPLICANT: LAX, Irit
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PTB domain of IRS-1
; OTHER INFORMATION: IRS-1
US-09-731-660A-2

Query Match      11.2%; Score 78; DB 9; Length 114;
Best Local Similarity 30.0%; Pred. No. 0.82;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDSNLSFESGRCQTGGIFAFKCAAEELFNNLQEIOMQNSINNVVEPVVERN 111
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Db 51 IRRCGHSENFFFIEVGRSAVTGPGBFMMQ-----VDDSVVAQN 88
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QY 112 NHQTELEVPR 121
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 89 MHETILEAMR 98
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 15
US-10-694-874-3
; Sequence 3, Application US/10694874
; Publication No. US20040097713A1
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 14, 2005, 03:11:53 ; Search time 224.079 Seconds
(without alignments)
949.290 Million cell updates/sec

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Perfect score: 696
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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6:	/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143.5	20.6	1446	3	US-08-787-091-1
2	137.5	19.8	1146	4	US-09-620-312D-854
3	135.5	19.3	1239	4	US-09-949-016-1713
4	134.5	19.3	531	4	US-09-270-767-26283
5	134.5	19.3	1363	4	US-09-270-767-10813
6	133.5	19.2	914	4	US-09-620-312D-855
7	124.5	17.9	2735	4	US-09-620-312D-842
c 8	100	14.4	601	4	US-09-949-016-59090
9	100	14.4	8291	4	US-09-949-016-13455
c 10	83	11.9	1813	3	US-09-453-702B-91
11	82.5	11.9	415	4	US-09-621-976-12526
12	79.5	11.4	2959	4	US-09-949-016-5549

13	79.5	11.4	16782	4	US-09-949-016-17291
14	79	11.4	1239	4	US-09-248-796A-6449
15	78	11.2	5828	4	US-09-023-655-1386
16	78	11.2	5828	4	US-09-903-248-6
17	78	11.2	5828	4	US-09-903-199-6
18	78	11.2	5828	4	US-09-903-216-6
19	78	11.2	5828	4	US-09-903-063-6
20	78	11.2	5828	4	US-09-859-604-6
21	78	11.2	6152	1	US-08-557-139-1
22	77.5	11.1	698	3	US-08-896-164-44
23	75	10.8	1600	2	US-08-531-439B-3
24	75	10.8	1600	4	US-09-023-655-1505
25	74.5	10.7	1000	4	US-09-270-767-2197
26	74.5	10.7	1461	4	US-09-270-767-11592
27	74.5	10.7	2209	4	US-09-489-847-16
28	74	10.6	1664976	4	US-08-916-421B-1
29	74	10.6	1664976	4	US-09-692-570-1
c 30	74	10.6	4403765	3	US-09-103-840A-2
c 31	74	10.6	4411529	3	US-09-103-840A-1
c 32	73.5	10.6	1299	4	US-09-891-641-49
33	73.5	10.6	1746	4	US-09-248-796A-1302
34	72.5	10.4	461	4	US-09-270-767-1052
35	72.5	10.4	461	4	US-09-270-767-11316
c 36	72.5	10.4	654	4	US-09-270-767-11316
37	72.5	10.4	1626	3	US-09-134-001C-1644
c 38	72.5	10.4	3086	4	US-09-710-279-3956
39	72	10.3	453	4	US-09-270-767-3433
40	72	10.3	453	4	US-09-270-767-18715
41	72	10.3	1896	4	US-09-949-016-5724
42	72	10.3	2313	3	US-09-370-838-157
43	72	10.3	2313	4	US-09-854-133-157
44	72	10.3	15062	3	US-09-004-838-89
45	71	10.2	12286	4	US-09-902-540-1035

ALIGNMENTS

RESULT 1
US-08-787-091-1
; Sequence 1, Application US/08787091
; Patent No. 6100386
; GENERAL INFORMATION:
; APPLICANT: Carpino, Nicholas A.
; APPLICANT: Kobayashi, Ryuji
; APPLICANT: Wisniewski, David G.
; APPLICANT: Strife, Annabel O'C.
; APPLICANT: Clarkson, Bayard D.
; TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in
; TITLE OF INVENTION: Chronic Myelogenous Leukemia
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,091
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,418
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-05pa


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Db 982 GAGCAGATTTACGAGCGGTCCACAGTGCACAGTCCACCTGCGCCATCGCAGAGCAGCACAGCGG 1041
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGlu---LeuGlu 118
Db 1042 GCTCTGCTGGAATGGAGAGAACGTGAGGCTGCTGAACAAGGGCAGGAACTTACTCG 1101
Qy 119 ValProArgThrProArgThr 125
Db 1102 TATCCTGTCACCCAGGACC 1122

RESULT 8
US-09-949-016-59090/c
; Sequence 59090, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59090
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59090

Alignment Scores:
Pred. No.: 0.000126 Length: 601
Score: 100.00 Matches: 26
Percent Similarity: 46.34% Conservative: 12
Best Local Similarity: 31.71% Mismatches: 26
Query Match: 14.37% Indels: 18
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-59090 (1-601)
Qy 62 PheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyLeuPheAlaPheLysCys 81
Db 462 TTTTCTTTGAGCGAGCGCGTCTGCTGCTGAGAGAGGCACTTTGAGTTGGAAC 403
Qy 82 AlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMet-----GlnAsnAsnSer 99
Db 402 CGGCAAGGCAATGAGATCTTCTGGCCCTGGAAGAGGCCATCTCTGCCAGAGAATGCT 343
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluVal 119
Db 342 GCACCGGTACACCCACCG-----CAGCCAGCCCAATCCCGCGTGGCTG 295
Qy 120 ProArg-----ThrProArgThrProThr 127
Db 294 CCGCGCGCTGATAGCCCTTACTCTGCGCGCATGACTCACTGCGCGCGCTTCACCACC 235
Qy 128 ThrPro 129
Db 234 ACACCG 229

RESULT 9
US-09-949-016-13455
; Sequence 13455, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59090
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59090

Alignment Scores:
Pred. No.: 0.000126 Length: 601
Score: 100.00 Matches: 26
Percent Similarity: 46.34% Conservative: 12
Best Local Similarity: 31.71% Mismatches: 26
Query Match: 14.37% Indels: 18
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-59090 (1-601)
Qy 62 PheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyLeuPheAlaPheLysCys 81
Db 462 TTTTCTTTGAGCGAGCGCGTCTGCTGCTGAGAGAGGCACTTTGAGTTGGAAC 403
Qy 82 AlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMet-----GlnAsnAsnSer 99
Db 402 CGGCAAGGCAATGAGATCTTCTGGCCCTGGAAGAGGCCATCTCTGCCAGAGAATGCT 343
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluVal 119
Db 342 GCACCGGTACACCCACCG-----CAGCCAGCCCAATCCCGCGTGGCTG 295
Qy 120 ProArg-----ThrProArgThrProThr 127
Db 294 CCGCGCGCTGATAGCCCTTACTCTGCGCGCATGACTCACTGCGCGCGCTTCACCACC 235
Qy 128 ThrPro 129
Db 234 ACACCG 229

RESULT 10
US-09-453-702B-91/c
; Sequence 91, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13455
; LENGTH: 8291
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13455

Alignment Scores:
Pred. No.: 0.00663 Length: 8291
Score: 100.00 Matches: 26
Percent Similarity: 46.34% Conservative: 12
Best Local Similarity: 31.71% Mismatches: 26
Query Match: 14.37% Indels: 18
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-13455 (1-8291)
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Db 5677 TTTTCTTTGAGCGAGCGCGTCTGCTGCTGAGAGAGGCACTTTGAGTTGGAAC 5736
Qy 82 AlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMet-----GlnAsnAsnSer 99
Db 5737 CGGCAAGGCAATGAGATCTTCTGGCCCTGGAAGAGGCCATCTCTGCCAGAGAATGCT 5796
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluVal 119
Db 5797 GCACCGGTACACCCACCG-----CAGCCAGCCCAATCCCGCGTGGCTG 5844
Qy 120 ProArg-----ThrProArgThrProThr 127
Db 5845 CCGCGCGCTGATAGCCCTTACTCTGCGCGCATGACTCACTGCGCGCGCTTCACCACC 5904
Qy 128 ThrPro 129
Db 5905 ACACCG 5910

RESULT 10
US-09-453-702B-91/c
; Sequence 91, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
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Db 1023 GAAAGTCTTACCTATTTCCACCAG-----AGGACCCACACTCGAGAAAAA--- 1070
QY 77 PheAlaPheLysCysAlaAlaGlnGluLeuPheAsnMetLeuGlnGlnIleMetGln 96
Db 1071 ---CCCTATGACTGTATCACTCTGGGAAAGCTTCAATCATATAAACAACCTCAATAAA 1127
QY 97 AsnAsnSerIleAsnValValGluGluProVal-----Val 108
Db 1128 CATGACGGAATTCATACAGAGAGAAACCTTATCTCTGTTCTCAGTGTGGAAAAAACTTC 1187
QY 109 GluArgAsnAsnHisGlnThrGluLeuGlu 118
Db 1188 CGTCAGAAATCTCATCGGAGTCGTCATGAA 1217

RESULT 13
US-09-949-016-17291
; Sequence 17291, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17291
; LENGTH: 16782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17291

Alignment Scores:
Pred. No.: 16.8 Length: 16782
Score: 79.50 Matches: 27
Percent Similarity: 45.38% Conservative: 32
Best Local Similarity: 20.77% Mismatches: 48
Query Match: 11.42% Indels: 23
DB: 4 Gaps: 6

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-17291 (1-16782)
QY 2 ThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGlyAsn 21
Db 12681 TCATTCCCAAAAAAGGAAATGAGAAATCTGTTAGTACCATTGAGATGAT----- 12734
QY 22 GluLeuGlySerGlyIleMetGluLeuThr-----AspThrGluLeuLeuTyr 38
Db 12735 -----ACTCCTAGAGGAACTCTCAAAATATGTAGACATCATGATTATTCGCCCTT 12785
QY 39 ThrArgLysArgAspSerValIleHisTyr-----LeuCysLeuArgArgTyrGly 56
Db 12786 ACTCGAAATCGGAGGACAGGAGATGGTACACTGTGCCACTGTGTGGGAAACAGTTTAAT 12845
QY 57 TyrAspSerAsnLeuPheSerPheGluSerGlyArgCysGlnThrGlyGlnGlyIle 76
Db 12846 GAAAGTCTTACCTCATTTCCACCAG-----AGGACCCACACTCGAGAAAAA--- 12893
QY 77 PheAlaPheLysCysAlaAlaGlnGluLeuPheAsnMetLeuGlnGlnIleMetGln 96
Db 12894 ---CCCTATGACTGTATCACTCTGGGAAAGCTTCAATCATATAAACAACCTCAATAAA 12950
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QY 97 AsnAsnSerIleAsnValValGluGluProVal-----Val 108
Db 12951 CATGACGGAATTCATACAGAGAGAAACCTTATCTGTCTCAGTGTGGAATAAACTTC 13010
QY 109 GluArgAsnAsnHisGlnThrGluLeuGlu 118
Db 13011 CGTCAGAAATCTCATCGGAGTCGTCATGAA 13040

RESULT 14
US-09-248-796A-6449
; Sequence 6449, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6449
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6449
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Alignment Scores:
Pred. No.: 0.386 Length: 1239
Score: 79.00 Matches: 32
Percent Similarity: 43.70% Conservative: 20
Best Local Similarity: 26.89% Mismatches: 47
Query Match: 11.35% Indels: 20
DB: 4 Gaps: 6
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US-09-757-415A-1_COPY_11_140 (1-130) x US-09-248-796A-6449 (1-1239)

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QY 10 LysPheLysValIleAsnValAspAspGlyAsn-----GluLeuGlySerGlyIle 27
Db 469 AAATTGAAAGTTTCAACGTTAACACATGACACATTCGACATTCGTTTGA 528
QY 28 MetGluLeuThrAspThrGluLeuLeuLeuThrArgLysArgAspSerValIleTyr 47
Db 529 CAAGAAGTCACATGACTATTGACATTTCTTATACGCTGMAAAGGTCGACGTT----- 582
QY 48 HisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe----- 62
Db 583 -----ATTTGAAACAATTTGACAGCTGCTAAGAACATTTGTTTACAAACAGTTAAC 633
QY 63 SerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 634 TCATTC---AGTGCTCAAACTTGACCATTCGACGTTTCATTCCTGTTCTTCTTGT 690
QY 83 ArgAlaGluGluLeuPheAsnMetLeuGlnGlnIleMetGlnAsnAsnSerIleAsnVal 102
Db 691 TCTGTTGAAAAAGTC-----GAACTTGCTGAATTGACTTCTATTGGT--- 732
QY 103 ValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValProArg 121
Db 733 ---AATTCTTACGATATCAACAAAATGATGACTTGAATGATTTCCCTNAA 786
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RESULT 15
US-09-023-655-1386
; Sequence 1386, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
```

/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

/ TITLE OF INVENTION: EXPRESSION

/ NUMBER OF SEQUENCES: 1508

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

/ STREET: 3174 PORTER DRIVE

/ CITY: PALO ALTO

/ STATE: CALIFORNIA

/ COUNTRY: USA

/ ZIP: 94304

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/023,655

/ FILING DATE: HEREWITH

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER:

/ FILING DATE:

/ CLASSIFICATION:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Zeller, Karen J.

/ REGISTRATION NUMBER: 37,071

/ REFERENCE/DOCKET NUMBER: PA-0001 US

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (650) 855-0555

/ TELEFAX: (650) 845-4166

/ INFORMATION FOR SEQ ID NO: 1386:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 5828 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ IMMEDIATE SOURCE:

/ LIBRARY: GENBANK

/ CLONE: G386256

/ US-09-023-655-1386

Alignment Scores:

Pred. No.:	5.58	Length:	5828
Score:	78.00	Matches:	21
Percent Similarity:	40.00%	Conservative:	7
Best Local Similarity:	30.00%	Mismatches:	20
Query Match:	11.21%	Indels:	22
DB:	4	Gaps:	1

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-023-655-1386 (1-5828)

QY	52	LeuAtgAtgTyrGlyTyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCysGln	71
Db	1651	ATCAGGCGGTGGGCCACCTCTTCTTCATCAGGTTGGCCGTTCTGCCGTG	1710
QY	72	ThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeu	91
Db	1711	ACGGGGCCCGGGGAGTTCTGGATGCAG-----	1737
QY	92	GlnGluIleMetGlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsn	111
Db	1738	-----GTGGATGACTCTGTGGTGGCCAGAAC	1764
QY	112	AsnHisGlnThrGluLeuGluValProArg	121
Db	1765	ATGCACGAGACCATCTCGAGGCCATGCCG	1794

Search completed: February 14, 2005, 03:23:22

Job time : 232.079 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 14, 2005, 03:17:13 ; Search time 715.855 Seconds
(without alignments)
1071.529 Million cell updates/sec

Title: US-09-757-415a-1_COPY_11_140
Perfect score: 696
Sequence: 1 DTVPDNRNKKFKVNVDDG.....NNHQTELEVPRTPTTTEG 130

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 295022984 residues
Total number of hits satisfying chosen parameters: 10757346
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool/US09757415/runat_07022005_160042_26863/app.query.fasta_1.526
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR_MAX=100
-MAXLEN=200000000 -USER=US09757415 @CNG 1.1 582 @runat_07022005_160042_26863
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	696	100.0	1532	15	US-10-146-473-27	Sequence 27, Appl
2	696	100.0	2074	17	US-10-276-774-842	Sequence 842, App
3	264.5	38.0	452	10	US-09-918-995-27390	Sequence 27390, A
4	143.5	20.6	1908	17	US-10-172-118-601	Sequence 601, App
5	143.5	20.6	1908	17	US-10-342-887-601	Sequence 601, App
6	143.5	20.6	1908	18	US-10-370-715B-49	Sequence 49, Appl
7	143.5	20.6	1972	17	US-10-240-425-380	Sequence 380, App
8	143.5	20.6	3809	13	US-10-001-870-68	Sequence 68, Appl
9	141	20.3	1539	9	US-09-789-919-15	Sequence 15, Appl
10	141	20.3	1850	9	US-09-789-919-57	Sequence 57, Appl
11	137.5	19.8	1146	15	US-10-037-270-854	Sequence 854, App
12	137.5	19.8	1146	17	US-10-117-722-854	Sequence 854, App
13	137.5	19.8	1750	17	US-10-307-928A-5	Sequence 5, Appl
14	135.5	19.5	1221	17	US-10-350-923B-37	Sequence 37, Appl
15	133.5	19.2	914	15	US-10-037-270-855	Sequence 855, App
16	133.5	19.2	914	17	US-10-117-722-855	Sequence 855, App
17	124.5	17.9	1951	13	US-10-098-841-102	Sequence 102, App
18	124.5	17.9	2000	10	US-09-814-353-21341	Sequence 21341, A
19	124.5	17.9	2305	18	US-10-723-860-5489	Sequence 5489, Ap
20	124.5	17.9	2735	15	US-10-037-270-842	Sequence 842, App
21	124.5	17.9	2735	17	US-10-117-722-842	Sequence 842, App
22	122	17.5	421	10	US-09-918-995-34825	Sequence 34825, A
23	120.5	17.3	2339	17	US-10-112-944-41	Sequence 41, Appl
24	113	16.2	508	10	US-09-918-995-24418	Sequence 24418, A
25	111.5	16.0	1385	15	US-10-106-698-1983	Sequence 1983, Ap
26	95.5	13.7	714	16	US-10-029-386-24084	Sequence 24084, A
27	95.5	13.7	804	16	US-10-029-386-24133	Sequence 24133, A
28	95.5	13.7	1409	17	US-10-264-049-165	Sequence 165, App
29	88	12.6	507	16	US-10-029-386-10377	Sequence 10377, A
30	85	12.2	24740	16	US-10-292-951-41	Sequence 41, Appl
31	85	12.2	24740	17	US-10-382-844-41	Sequence 41, Appl
32	83	11.9	1813	14	US-10-114-170-91	Sequence 91, Appl
33	78	11.2	5800	18	US-10-735-512-28	Sequence 28, Appl
34	78	11.2	5828	9	US-09-903-248-6	Sequence 6, Appl
35	78	11.2	5828	9	US-09-959-604-6	Sequence 6, Appl
36	78	11.2	5828	9	US-09-903-063-6	Sequence 6, Appl
37	78	11.2	5828	9	US-09-903-216-6	Sequence 6, Appl
38	78	11.2	5828	9	US-09-903-199-6	Sequence 6, Appl
39	78	11.2	5828	9	US-09-880-107-3021	Sequence 3021, Ap
40	78	11.2	5828	9	US-09-903-023-6	Sequence 6, Appl
41	78	11.2	5828	10	US-09-436-184-6	Sequence 6, Appl
42	78	11.2	5828	17	US-10-172-118-1165	Sequence 1165, Ap
43	78	11.2	5828	17	US-10-342-887-1165	Sequence 1165, Ap
44	78	11.2	5828	17	US-10-641-643-1386	Sequence 1386, Ap
45	78	11.2	6321	17	US-10-334-143-155	Sequence 155, App

ALIGNMENTS

RESULT 1
US-10-146-473-27
; Sequence 27, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27

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; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-27

Alignment Scores:
Pred. No.: 1,12e-89 Length: 1532
Score: 696.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-757-415A-1_COPY_11_140 (1-130) x US-10-146-473-27 (1-1532)

QY 1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly 20
   |||||
Db 36 GACACTGTCCCAAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGGG 95

QY 21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuThrArg 40
   |||||
Db 96 AATGATTAGGTTCTGGCATATATGGAACCTTACAGACAGAACTGATTTTATACACCCG 155

QY 41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
   |||||
Db 156 AAACGTGACTCAGTAAATGGCACTACCTCTGCTCGCAGCGCTATGGCTATGACTCGAAT 215

QY 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
   |||||
Db 216 CTCCTTTCTTTTGAAGTGGTGAAGGTGTCAAACTGGACAAGGAATCTTTTGCCTTTAAG 275

QY 81 CysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSerIle 100
   |||||
Db 276 TGTGCCCGTGCAGAGAATTTTAAACATGTTGCAAGAGATTATGCCAAATATATAGTATA 335

QY 101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
   |||||
Db 336 AATGTGTGGAAGAGCCAGTTGTAGAAAGAAATAATCATCAGACAGAAATTGGAAGTCCCT 395

QY 121 ArgThrProArgThrProThrThrProGly 130
   |||||
Db 396 AGAACACCTCGAACACCTCAACTCCAGGA 425

RESULT 2
US-10-276-774-842
; Sequence 842, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 842
; LENGTH: 2074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-842

Alignment Scores:
Pred. No.: 1,76e-89 Length: 2074
Score: 696.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
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US-09-757-415A-1_COPY_11_140 (1-130) x US-10-276-774-842 (1-2074)

QY 1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly 20
   |||||
Db 575 GACACTGTCCCAAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGGG 634

QY 21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuThrArg 40
   |||||
Db 635 AATGATTAGGTTCTGGCATATATGGAACCTTACAGACAGAACTGATTTTATACACCCG 694

QY 41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
   |||||
Db 695 AAACGTGACTCAGTAAATGGCACTACCTCTGCTCGCAGCGCTATGGCTATGACTCGAAT 754

QY 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
   |||||
Db 755 CTCCTTTCTTTTGAAGTGGTGAAGGTGTCAAACTGGACAAGGAATCTTTTGCCTTTAAG 814

QY 81 CysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSerIle 100
   |||||
Db 815 TGTGCCCGTGCAGAGAATTTTAAACATGTTGCAAGAGATTATGCCAAATATATAGTATA 874

QY 101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
   |||||
Db 875 AATGTGTGGAAGAGCCAGTTGTAGAAAGAAATAATCATCAGACAGAAATTGGAAGTCCCT 934

QY 121 ArgThrProArgThrProThrThrProGly 130
   |||||
Db 935 AGAACACCTCGAACACCTACACTCCAGGA 964

RESULT 3
US-09-918-995-27390
; Sequence 27390, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27390
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27390

Alignment Scores:
Pred. No.: 4,37e-28 Length: 452
Score: 264.50 Matches: 49
Percent Similarity: 84.72% Conservative: 12
Best Local Similarity: 68.06% Mismatches: 10
Query Match: 38.00% Indels: 1
DB: 10 Gaps: 1

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-918-995-27390 (1-452)

QY 60 AsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPhe 79
   |||||
Db 42 CACCTCTTCTCTTTGAGAGTGGCCCGCATGTGCAGACAGCCCATGGATATTTGCATTT 101

QY 80 LysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSer 99
   |||||
Db 102 AAGTGTTCCTCCGCGCTGAGGAATCTTCAACCTCTCTCAGGATCTGTGATGCGTGCACAGC 161
```



```
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: Related Diseases
; CURRENT APPLICATION NUMBER: P1948R1-US
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 49
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-49
Alignment Scores:
Pred. No.: 1.18e-09 Length: 1908
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservative: 20
Best Local Similarity: 29.46% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 18 Gaps: 2
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QY 24 GlySerGlyLeuMetGluLeuThrAspThrGluLeuLeuLeuLeuTyrThrArgLysArgAsp 43
Db 536 GGCTCTACGTGCTGAGGTGTGAGGCTGAAAGGCTGACTCTCTGACCGTGGGGGCCAG 595
QY 44 Ser-----VallystTrpHisTyrLeuCysLeuArgArgTyrGlyTyr 57
Db 596 AGTCAGATACTGGAGCCACTCTCTGCTGCGCCCTACACTCTGTGGTGGCTATGGCCGG 655
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePhe 77
Db 656 GACAAGTCTATGTTCTCTTCGAGGCGCGCGCGCTGCGCCCTCAGGCGCTCGAACCTTC 715
QY 78 AlaPheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsn 97
Db 716 ACCTCCAGCGCACAGGAAATGACATCTCTCAGGCGGCGCGCTGCGCCCTCAGGCGCTCGAACCTTC 871
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnAsnHisGln 114
Db 776 CAGAGGCCCGCAGGAAAGCGGACAGGCGGCGAGGCTGTTCTCAGAGCTGACTCCCATGAA 835
QY 115 ThrGluLeuGluValProArgThrProArgThrPro 126
Db 836 GGGGAGGTGGCAGAGGGAAGTTGCTTCCCACT 871
RESULT 7
US-10-240-425-380
; Sequence 380, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 380
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; LENGTH: 1972
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF035299
US-10-240-425-380
Alignment Scores:
Pred. No.: 1.24e-09 Length: 1972
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservative: 20
Best Local Similarity: 29.46% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 17 Gaps: 2
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QY 24 GlySerGlyLeuMetGluLeuThrAspThrGluLeuLeuLeuLeuTyrThrArgLysArgAsp 43
Db 600 GGCTCTACGTGCTGAGGTGTGAGGCTGAAAGGCTGACTCTCTGACCGTGGGGGCCAG 659
QY 44 Ser-----VallystTrpHisTyrLeuCysLeuArgArgTyrGlyTyr 57
Db 660 AGTCAGATACTGGAGCCACTCTCTGCTGCGCCCTACACTCTGTGGTGGCTATGGCCGG 719
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePhe 77
Db 720 GACAAGTCTATGTTCTCTTCGAGGCGCGCGCTGCGCCCTCAGGCGCTCGAACCTTC 779
QY 78 AlaPheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsn 97
Db 780 ACCTCCAGCGCACAGGAAATGACATCTCTCAGGCGGAGTTGAGACTGCCATCCACCGG 839
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnAsnHisGln 114
Db 840 CAGAGGCCCGCAGGAAAGCGGACAGGCGGCGAGGCTGTTCTCAGAGCTGACTCCCATGAA 899
QY 115 ThrGluLeuGluValProArgThrProArgThrPro 126
Db 900 GGGGAGGTGGCAGAGGGAAGTTGCTTCCCACT 935
RESULT 8
US-10-001-870-68
; Sequence 68, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 3809
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-870-68
Alignment Scores:
Pred. No.: 3.33e-09 Length: 3809
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservative: 20
Best Local Similarity: 29.46% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 13 Gaps: 2
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US-09-757-415A-1_COPY_11_140 (1-130) x US-10-001-870-68 (1-3809)
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
Db 2397 GGCTCTACGTCTGGAGGCTGAAAGGCTGACTCTCTGACCGTGGGGGCCAG 2456
QY 44 Ser-----ValIleTIPHisTyrLeuCysLeuArgArgTyrGlyTyr 57
Db 2457 AGTCAGACTAGGACCACTCTCTGCTGCCCTACACTCTGTTCCTGCTGCTATGGCCG 2516
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePhe 77
Db 2517 GACAAGTCTATCTCTTCGAGGCGCGCGCTGCCCTCAGCGCCCTGGAACCTTC 2576
QY 78 AlaPheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsn 97
Db 2577 ACCTTCAGACGGCAGGGAATGACATCTCCAGGCAGTTGAGACTGCCACCCGG 2636
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnAsnHisGln 114
Db 2637 CAGAGGCCCGAGGAAGCGGACAGGGGCAGATGTTCTCAGAGCTGACTCCCATGAA 2696
QY 115 ThrGluLeuValProArgThrProArgThrPro 126
Db 2697 GGGAGGTGCGACAGGGGAAGTTGCCCTTCCCCACCT 2732
RESULT 9
US-09-789-919-15
; Sequence 15, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; APPLICANT: Moore, Kateri
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789, 919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-789-919-15
Alignment Scores:
Pred. No.: 1.97e-09 Length: 1539
Score: 141.00 Matches: 36
Percent Similarity: 44.09% Conservative: 20
Best Local Similarity: 28.35% Mismatches: 47
Query Match: 20.26% Indels: 24
DB: Gaps: 3
US-09-757-415A-1_COPY_11_140 (1-130) x US-09-789-919-15 (1-1539)
QY 23 LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42
Db 560 CTGGCCCAAGATGACATCCAACTGAGGGAGACA-----TCCAAGCCCCAG 604
QY 43 AspSerValIleTIPHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe 62
Db 605 GCCTGTTTAGTGGCCCTACCGTTTCCTGCGCAAGTACGGCTCTGACAAGGGTGTGTTTC 664
QY 63 SerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 665 TCGTTTGGAGCTGGCGCGCTGTGACTCAGGTGAGGGCTTTTTCCTTCAGTAGCCCG 724
QY 83 ArgAlaGluLeuPheAsnMetGluGlnIleMetGlnAsnSerIleAsnVal 102
Db 725 CGTGCCCCAGACATATGTGGGTGTGTGGCTGCGCCATTGCCCGCCAGCGGAGCGTCTT 784
QY 103 ValGlu----- 104
US-09-789-919-15
; Sequence 15, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; APPLICANT: Moore, Kateri
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789, 919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-789-919-57
Alignment Scores:
Pred. No.: 2.18e-09 Length: 1650
Score: 141.00 Matches: 36
Percent Similarity: 44.09% Conservative: 20
Best Local Similarity: 28.35% Mismatches: 47
Query Match: 20.26% Indels: 24
DB: Gaps: 3
US-09-757-415A-1_COPY_11_140 (1-130) x US-09-789-919-57 (1-1650)
QY 23 LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42
Db 671 CTGGCCCAAGATGACATCCAACTGAGGGAGACA-----TCCAAGCCCCAG 715
QY 43 AspSerValIleTIPHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe 62
Db 716 GCCTGTTTAGTGGCCCTACCGTTTCCTGCGCAAGTACGGCTCTGACAAGGGTGTGTTTC 775
QY 63 SerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 776 TCGTTTGGAGCTGGCGCGCTGTGACTCAGGTGAGGGCTTTTTCCTTCAGTAGCCCG 835
QY 83 ArgAlaGluLeuPheAsnMetGluGlnIleMetGlnAsnSerIleAsnVal 102
Db 836 CGTGCCCCAGACATATGTGGGTGTGTGGCTGCGCCATTGCCCGCCAGCGGAGCGTCTT 895
QY 103 ValGlu----- 104
Db 896 CCAGAGCTGGCCATGTCACCCACCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTA 955
QY 105 GluProValValGluArgAsnAsnHisGlnThrGluLeuGluValProArgThrProArg 124
Db 956 GAGCCCCCTGGAGAGCTTCGGGAGGTGGGCCCGCCAGGATTTGAGCTGCCCACTCCAGAAAG 1015
QY 125 ThrPro---ThrThrProGly 130
Db 1016 CTGGCTCTTAACATGATCCCGGG 1036
RESULT 11
US-10-037-270-854
; Sequence 854, Application US/10037270
; Publication No. US20030104529A1
```


APPLICANT: Burgees, Catherine E.
APPLICANT: Catterton, Elina
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Ji, Weizhen
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; Publication No. US2004002084A1
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Ma, Xiao Jun
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from active
; FILE REFERENCE: S03157-01
; CURRENT APPLICATION NUMBER: US/10/307,928A
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,495
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/383,744
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/384,024
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/401,788
; PRIOR FILING DATE: 2002-08-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Curation version 0.1
; SEQ ID NO 5
; LENGTH: 1750
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(1189)
US-10-307-928A-5
Alignment Scores:
Pred. No.: 7 64e-09 Length: 1750
Score: 137.50 Matches: 34
Percent Similarity: 49.07% Conservative: 19
Best Local Similarity: 31.48% Mismatches: 42
Query Match: 19.76% Indels: 13
DB: 17 Gaps: 3
US-09-757-415A-1_COPY_11_140 (1-130) x US-10-307-928A-5 (1-1750)
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleuTyrThrArgLysArgAsp 43
Db 653 GGTGAATGCACATGCAGATCATGAAATATCTATCTCTGGATATCCAAATGCC 712
QY 44 SerValLys-----TrpHisTyrLeuCysLeuArgGlyTyrAspSerAsn 60
Db 713 AAGGTCAAATGGTGTGTGGCCCTCTCAGCTCAGTGAAGAGATACGTCGGGACTCAAG 772
QY 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
Db 773 TGGTTCACGTTTGAAGTCAAGAAAGATGTGTGACACAGGAGGAGGACTATCTACTTTTCAA 932

QY 81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMetGlnAsnSerIle 100
Db 833 ACAAGGGAAGAGAA-----ATGATCTATCAGAAAGTTTCATCTCGGACACTG 880
QY 101 AsnValValGluGlu-----ProValValGluArgAsnAsnHisGln 114
Db 881 GCCATAGCTGAGCAACATGAAGATTAACTAGTAATGAACAGAGCCCGCTTCAG 940
QY 115 ThrGluLeuGluValProArgThr 122
Db 941 ACAAGCTTGACTGAACCAATGACA 964

RESULT 14

US-10-350-923B-37
; Sequence 37, Application US/10350923B
; Publication No. US2004002084A1
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Ma, Xiao Jun
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from active
; FILE REFERENCE: S03157-01
; CURRENT APPLICATION NUMBER: US/10/350,923B
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US/ 09/454,280
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: PCT/US99/28773
; PRIOR FILING DATE: 1999-06-12
; PRIOR APPLICATION NUMBER: US 60/111,006
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 37
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-350-923B-37

Alignment Scores:

Pred. No.: 8 67e-09 Length: 1221
Score: 135.50 Matches: 37
Percent Similarity: 49.07% Conservative: 16
Best Local Similarity: 34.26% Mismatches: 35
Query Match: 19.47% Indels: 20
DB: 17 Gaps: 4

US-09-757-415A-1_COPY_11_140 (1-130) x US-10-350-923B-37 (1-1221)

QY 38 TyrThrArgLysArgAsp---SerValLys-TrpHisTyrLeuCysLeuArgArgTyrGln 56
Db 348 TGGGCCCGAGCCAGGAGCCAGCTGTACACTGGCCCTACAGGTTTCTCGCGGCTTTGG 407
QY 56 TyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGly 76
Db 408 GCGGACAAAGGTAACTCTTTCTTTGAGCGAGCGCGCTCGCTCTCTGGAGAGGGCAA 467
QY 76 ePheAlaPheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMet-- 95
Db 468 CTTTGAAGTTTCAACCCCGGCAAGGCAATGAGATCTTTTGGCCCTTGAAGAGGCCATCTC 527
QY 96 ----GlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsnHisGln 114
Db 528 TGCCCAAGAAATGTGACCCCGCTACACCCCAACCG-----CAGCCAGCCAC 575
QY 114 nThrGluLeuGluValProArg-----Th 122
Db 576 AATCCCGCGCTCGCTCGCCCGCCCTAGTACCCCTACTCTCGGCCGCGATGACTACTGCC 635
QY 122 rProArgThrProThrPro 129
Db 636 GCGGCTTCACCCACCACACCG 657

RESULT 15

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US-10-037-270-855
; Sequence 855, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghaast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1e1 Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: dt_FL_genes Version 1.0
; SEQ ID NO 855
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(867)
US-10-037-270-855
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Alignment Scores:

Pred. No.:	1,09e-08	Length:	914
Score:	133.50	Matches:	33
Percent Similarity:	48.62%	Conservative:	20
Best Local Similarity:	30.28%	Mismatches:	43
Query Match:	19.18%	Indels:	13
DB:	15	Gaps:	3

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QY	24	GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp	43
DB	565	GGTGAATGCACATGCAGATCACTATGAAATATCTCTCTGGGATATCCACAATGCC	624
QY	44	SerValIys-----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn	60
DB	625	AGGTCAAACTGGTGATGTGGCTCTCAGCTCACTGAGGAGATACGGTCGGGACTCAACG	684
QY	61	LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys	80
DB	685	TGGTTTCACGTTTGAGTCAGGAAGAAATGTGTGACACAGGAGAGAACTATTCTCTTTCAA	744
QY	81	CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMetGlnAsnSerIle	100
DB	745	ACAAGGGAAGGAGAA-----ATGATCTATCAGAAGGTTTCATTCTCGCACACTG	792
QY	101	AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro	120
DB	793	GCCTAGCTGAGCAA-----CATGAAGATTAAATGCTAGAAATGGAA	834
QY	121	ArgThrProArgThrProThrPro	129

Db 835 CAGAAGGCCCGGTAAAGGCCCTTCCT 861

Search completed: February 14, 2005, 05:17:58
Job time : 827.855 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 02:44:53 ; Search time 5.06579 Seconds
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Title: US-09-757-415a-3
Perfect score: 107
Sequence: 1 HSQMAVHKLAKSIPLRRQVTVS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	729	1	US-07-640-029-3
2	107	100.0	731	1	US-07-921-807B-5
3	107	100.0	731	1	US-08-441-944A-5
4	107	100.0	731	3	US-08-439-992A-3
5	107	100.0	733	1	US-07-640-029-4
6	107	100.0	733	1	US-07-921-807B-6
7	107	100.0	733	1	US-08-441-944A-6
8	107	100.0	733	1	US-08-439-992A-4
9	107	100.0	816	1	US-07-640-029-1
10	107	100.0	817	1	US-07-640-029-2
11	107	100.0	820	1	US-07-921-807B-3
12	107	100.0	820	1	US-08-441-944A-3
13	107	100.0	820	1	US-08-166-717D-6
14	107	100.0	820	3	US-08-439-992A-1
15	107	100.0	822	1	US-07-997-133-1
16	107	100.0	822	1	US-07-921-807B-4
17	107	100.0	822	1	US-08-459-296-2
18	107	100.0	822	1	US-08-441-944A-4
19	107	100.0	822	2	US-08-451-822A-12
20	107	100.0	822	3	US-08-439-992A-2
21	107	100.0	822	3	US-08-323-430-12
22	101	94.4	609	4	US-09-949-016-7747
23	101	94.4	609	4	US-09-949-016-7748
24	101	94.4	609	4	US-09-949-016-7749
25	101	94.4	609	4	US-09-949-016-7750
26	101	94.4	609	4	US-09-949-016-7751
27	101	94.4	609	4	US-09-949-016-7752

28	101	94.4	609	4	US-09-949-016-7753	Sequence 7753, Ap
29	101	94.4	609	4	US-09-949-016-7754	Sequence 7754, Ap
30	83	77.6	643	1	US-08-471-570-6	Sequence 6, Appli
31	83	77.6	769	1	US-08-471-570-8	Sequence 8, Appli
32	83	77.6	821	2	US-08-451-822A-13	Sequence 13, Appli
33	83	77.6	821	3	US-08-323-430-13	Sequence 13, Appli
34	81	75.7	729	1	US-08-070-165F-6	Sequence 6, Appli
35	81	75.7	729	2	US-08-885-418-6	Sequence 6, Appli
36	81	75.7	731	1	US-08-070-165F-10	Sequence 10, Appli
37	81	75.7	731	2	US-08-885-418-10	Sequence 10, Appli
38	77	72.0	471	4	US-09-949-016-9042	Sequence 9042, Ap
39	77	72.0	471	4	US-09-949-016-9043	Sequence 9043, Ap
40	77	72.0	471	4	US-09-949-016-9044	Sequence 9044, Ap
41	77	72.0	471	4	US-09-949-016-9045	Sequence 9045, Ap
42	77	72.0	471	4	US-09-949-016-9046	Sequence 9046, Ap
43	77	72.0	471	4	US-09-949-016-9047	Sequence 9047, Ap
44	77	72.0	471	4	US-09-949-016-9048	Sequence 9048, Ap
45	77	72.0	471	4	US-09-949-016-9049	Sequence 9049, Ap

ALIGNMENTS

RESULT 1
US-07-640-029-3
; Sequence 3, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Valenzuela, Pablo D.T.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/640,029
; FILING DATE: 19910111
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: CH-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-640-029-3

Query Match 100.0%; Score 107; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22

Db 316 HSQMAVHKLAKSIPLRRQVTVS 337

RESULT 2
US-07-921-807B-5
; Sequence 5, Application US/07921807B
; Patent No. 5474914
; GENERAL INFORMATION:
; APPLICANT: SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
; TITLE OF INVENTION: OF VIRAL PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCLUNG, BARBARA G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0209.001
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-921-807B-5
Query Match 100.0%; Score 107; DB 1; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 318 HSQMAVHKLAKSIPLRRQVTVS 339
RESULT 3
US-08-441-944A-5
; Sequence 5, Application US/08441944A
; Patent No. 5767250
; GENERAL INFORMATION:
; APPLICANT: SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
; TITLE OF INVENTION: OF VIRAL PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,944A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,807
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCLUNG, BARBARA G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0209.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-944A-5
Query Match 100.0%; Score 107; DB 1; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 318 HSQMAVHKLAKSIPLRRQVTVS 339
RESULT 4
US-08-439-992A-3
; Sequence 3, Application US/08439992A
; Patent No. 6255454
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Pablo, Valenzuela D.T.
; APPLICANT: Philip, Barry J.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,992A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 0165.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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/ GENERAL INFORMATION:
/ APPLICANT: SPAETS, RICHARD
/ TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
/ TITLE OF INVENTION: OF VIRAL PROTEINS
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/

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PRIOR APPLICATION DATA: US 07/921,807
 APPLICATION NUMBER: 29-SEP-1992
 FILING DATE: ATTORNEY/AGENT INFORMATION:
 NAME: MCCLUNG, BARBARA G.
 REGISTRATION NUMBER: 33,113
 REFERENCE/DOCKET NUMBER: 0209.001
 TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: (510) 601-2708
/ TELEFAX: (510) 655-3542
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 733 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-441-944A-6

Query Match 100.0%; Score 107; DB 1; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 320 HSQMAVHKLAKSIPLRRQVTVS 341

RESULT 8
US-08-439-992A-4
/ Sequence 4, Application US/08439992A
/ Patent No. 6255454
/ GENERAL INFORMATION:
/ APPLICANT: Kiefer, Michael C.
/ APPLICANT: Pablo, Valenzuela D.T.
/ APPLICANT: Philip, Barr J.
/ TITLE OF INVENTION: Expression and Use of Human Fibroblast
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94608
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/439,992A
/ FILING DATE: 12-MAY-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Chung, Ling-Fong
/ REGISTRATION NUMBER: 36,482
/ REFERENCE/DOCKET NUMBER: 0165.004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 510-923-2704
/ TELEFAX: (510) 655-3542
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 733 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-439-992A-4

Query Match 100.0%; Score 107; DB 3; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 320 HSQMAVHKLAKSIPLRRQVTVS 341

RESULT 9
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US-07-640-029-1
/ Sequence 1, Application US/07640029
/ Patent No. 5229501
/ GENERAL INFORMATION:
/ APPLICANT: Kiefer, Michael C.
/ APPLICANT: Valenzuela, Pablo D.T.
/ APPLICANT: Barr, Philip J.
/ TITLE OF INVENTION: Expression and Use of Human Fibroblast
/ TITLE OF INVENTION: Growth Factor Receptor
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94608
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/640,029
/ FILING DATE: 19910111
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcclung, Barbara G.
/ REGISTRATION NUMBER: 33,113
/ REFERENCE/DOCKET NUMBER: CH-165
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 510-601-2708
/ TELEFAX: 510-655-3542
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 816 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-07-640-029-1

Query Match 100.0%; Score 107; DB 1; Length 816;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 404 HSQMAVHKLAKSIPLRRQVTVS 425

RESULT 10
US-07-640-029-2
/ Sequence 2, Application US/07640029
/ Patent No. 5229501
/ GENERAL INFORMATION:
/ APPLICANT: Kiefer, Michael C.
/ APPLICANT: Valenzuela, Pablo D.T.
/ APPLICANT: Barr, Philip J.
/ TITLE OF INVENTION: Expression and Use of Human Fibroblast
/ TITLE OF INVENTION: Growth Factor Receptor
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94608
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/07/640,029
;; APPLICATION NUMBER: 530
;; FILING DATE: 19910111
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McClung, Barbara G.
;; REGISTRATION NUMBER: 33,113
;; REFERENCE/DOCKET NUMBER: CH-165
;; TELEPHONE: 510-601-2708
;; TELEFAX: 510-655-3542
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 817 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-07-640-029-2

Query Match 100.0%; Score 107; DB 1; Length 817;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 11
US-07-921-807B-3
; Sequence 3, Application US/07921807B
; Patent No. 5474914
; GENERAL INFORMATION:
; APPLICANT: SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,807B
; FILING DATE: 29-SEP-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCLUNG, BARBARA G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0209.001
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; SEQUENCE CHARACTERISTICS:
; LENGTH: 820 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-921-807B-3

Query Match 100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 12
US-08-441-944A-3
; Sequence 3, Application US/08441944A
; Patent No. 5767250
; GENERAL INFORMATION:
; APPLICANT: SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,944A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,807
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCLUNG, BARBARA G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0209.001
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 820 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-944A-3

Query Match 100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 13
US-08-166-717D-6
; Sequence 6, Application US/08166717D
; Patent No. 5789182
; GENERAL INFORMATION:
; APPLICANT: Yavon, Avner
; APPLICANT: Ornitz, David M.
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
; TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
; FACTOR RECEPTOR
; NUMBER OF SEQUENCES: 6

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/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Clark & Elbing LLP
/ STREET: 176 Federal Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM COMPATIBLE
/ OPERATING SYSTEM: WINDOWS 95
/ SOFTWARE: WordPerfect (Version 7.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/166,717D
/ FILING DATE: 12/14/93
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/631,717
/ FILING DATE: 12/20/90
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kristina Bieker-Brady
/ REGISTRATION NUMBER: 39,109
/ REFERENCE/DOCKET NUMBER: 00383/017002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 723-4123
/ TELEFAX: (617) 723-8962
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 820
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-166-717D-6

Query Match 100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 14
US-08-439-992A-1
/ Sequence 1, Application US/08439992A
/ Patent No. 6255454
/ GENERAL INFORMATION:
/ APPLICANT: Kiefer, Michael C.
/ APPLICANT: Pablo, Valenzuela D.T.
/ TITLE OF INVENTION: Expression and Use of Human Fibroblast
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94608
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/439,992A
/ FILING DATE: 12-MAY-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Chung, Ling-Pong

Query Match 100.0%; Score 107; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;

/ REGISTRATION NUMBER: 36,482
/ REFERENCE/DOCKET NUMBER: 0165.004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 510-923-2704
/ TELEFAX: (510) 655-3542
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 820 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-439-992A-1

Query Match 100.0%; Score 107; DB 3; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 15
US-07-997-133-1
/ Sequence 1, Application US/07997133
/ Patent No. 5288855
/ GENERAL INFORMATION:
/ APPLICANT: Bergonzoni, Laura
/ APPLICANT: Mazue, Guy
/ APPLICANT: Isacchi, Antonella
/ APPLICANT: Roncucci, Romeo
/ APPLICANT: Sarmientos, Paolo
/ TITLE OF INVENTION: Extracellular Form of the Human
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
/ STREET: 1755 Jefferson Davis Highway, Fourth Floor
/ CITY: Arlington
/ STATE: Virginia
/ ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/997,133
/ FILING DATE: 28-DEC-1992
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/642,755
/ FILING DATE: 18-JAN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oblon, No. 5288855man F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 769-226-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 521-4500
/ TELEFAX: (703) 486-2347
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 822 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-07-997-133-1

Query Match 100.0%; Score 107; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRQVTVS 22
| | | | | | | | | | | | | | | |
Db 409 HSQMAVHKLAKSIPLRQVTVS 430

Search completed: February 14, 2005, 03:11:50
Job time : 5.06579 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 03:10:48 ; Search time 13.3158 Seconds
(without alignments)
539.846 Million cell updates/sec

Title: US-09-757-415A-3

Perfect score: 107

Sequence: 1 HSQMAVHKLAKSIPLRRQVTVS 22

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Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	100.0	22	10	US-09-757-415A-3
2	107	100.0	702	9	US-09-805-020-47
3	107	100.0	735	15	US-10-307-817-6
4	107	100.0	764	9	US-09-925-302-714
5	107	100.0	764	10	US-09-925-302-714
6	107	100.0	820	15	US-10-302-812-42
7	107	100.0	822	10	US-09-757-415A-2
8	107	100.0	822	14	US-10-204-041-2
9	107	100.0	822	15	US-10-394-322A-26
10	107	100.0	822	15	US-10-307-817-8
11	107	100.0	824	15	US-10-307-817-4
12	101	94.4	451	13	US-10-087-192-381
13	101	94.4	609	13	US-10-087-192-384

14	83	77.6	821	15	US-10-394-322A-27	Sequence 27, Appl
15	83	77.6	821	15	US-10-302-812-44	Sequence 44, Appl
16	83	77.6	822	16	US-10-648-593-254	Sequence 254, App
17	77	72.0	471	13	US-10-087-192-1134	Sequence 1134, Ap
18	64	59.8	20	14	US-10-199-820-247	Sequence 247, App
19	47	43.9	3588	16	US-10-741-601-378	Sequence 378, App
20	47	43.9	3588	17	US-10-741-601-1104	Sequence 1104, Ap
21	47	43.9	4346	16	US-10-741-601-377	Sequence 377, App
22	47	43.9	4346	17	US-10-741-600-1103	Sequence 1103, Ap
23	47	43.9	4347	16	US-10-741-601-376	Sequence 376, App
24	47	43.9	4347	17	US-10-741-600-1102	Sequence 1102, Ap
25	47	43.9	4370	16	US-10-408-765A-1267	Sequence 1267, Ap
26	47	43.9	4393	15	US-10-231-956A-366	Sequence 366, App
27	47	43.9	4393	17	US-10-741-600-1105	Sequence 1105, Ap
28	44	41.1	63	16	US-10-437-963-145357	Sequence 145357,
29	44	41.1	95	15	US-10-424-599-227789	Sequence 227789,
30	44	41.1	194	9	US-09-738-626-3731	Sequence 3731, Ap
31	44	41.1	214	15	US-10-424-599-227795	Sequence 227795,
32	44	41.1	234	15	US-10-424-599-227788	Sequence 227788,
33	44	41.1	1520	14	US-10-017-161-718	Sequence 718, App
34	44	41.1	1520	15	US-10-292-798-630	Sequence 630, App
35	43.5	40.7	60	16	US-10-437-963-115591	Sequence 115591,
36	43	40.2	40	15	US-10-424-599-203535	Sequence 203535,
37	43	40.2	152	15	US-10-424-599-150884	Sequence 150884,
38	43	40.2	152	16	US-10-437-963-116361	Sequence 116361,
39	43	40.2	155	16	US-10-767-701-58588	Sequence 58588, A
40	43	40.2	207	16	US-10-437-963-155843	Sequence 155843,
41	43	40.2	277	15	US-10-282-122A-51737	Sequence 51737, A
42	43	40.2	277	15	US-10-358-448A-8	Sequence 8, Appli
43	43	40.2	339	15	US-10-369-493-16476	Sequence 16476, A
44	43	40.2	446	15	US-10-282-122A-77108	Sequence 77108, A
45	43	40.2	778	16	US-10-437-963-118289	Sequence 118289,

ALIGNMENTS

RESULT 1

US-09-757-415A-3

Sequence 3, Application US/09757415A

Publication No. US20030040612A1

GENERAL INFORMATION:

APPLICANT: Zhou, Ming-Ming

TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor

FILE REFERENCE: 2459-1-002N

CURRENT APPLICATION NUMBER: US/09/757.415A

CURRENT FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/175867

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 22

TYPE: PRT

ORGANISM: Mus musculus

US-09-757-415A-3

Query Match 100.0%; Score 107; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22
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Db 1 HSQMAVHKLAKSIPLRRQVTVS 22

RESULT 2

US-09-805-020-47

Sequence 47, Application US/09805020

Publication No. US20020086384A1

GENERAL INFORMATION:

APPLICANT: LEVINE, Zurit

TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES

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; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-020-47

Query Match      100.0%; Score 107; DB 9; Length 702;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 3
US-10-307-817-6
; Sequence 6, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-6

Query Match      100.0%; Score 107; DB 15; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      322 HSQMAVHKLAKSIPLRRQVTVS 343

RESULT 4
US-09-925-302-714
; Sequence 714, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 714
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-714

Query Match      100.0%; Score 107; DB 10; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      351 HSQMAVHKLAKSIPLRRQVTVS 372

RESULT 5
US-09-925-302-714
; Sequence 714, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 714
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-714

Query Match      100.0%; Score 107; DB 9; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      351 HSQMAVHKLAKSIPLRRQVTVS 372

RESULT 6
US-10-302-812-42
; Sequence 42, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
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; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-42

Query Match      100.0%; Score 107; DB 15; Length 820;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 7
US-09-757-415A-2
; Sequence 2, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757,415A
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-757-415A-2

Query Match      100.0%; Score 107; DB 10; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 8
US-10-204-041-2
; Sequence 2, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTADINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 01111858.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/EP02/05420
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-204-041-2

Query Match      100.0%; Score 107; DB 14; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 9
US-10-394-322A-26
; Sequence 26, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-26

Query Match      100.0%; Score 107; DB 15; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 10
US-10-307-817-8
; Sequence 8, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 8
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-8

Query Match      100.0%; Score 107; DB 15; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 11
US-10-307-817-4
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; Sequence 4, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-4

Query Match      100.0%; Score 107; DB 15; Length 824;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      411 HSQMAVHKLAKSIPLRRQVTVS 432

RESULT 12
US-10-087-192-381
; Sequence 381, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 381
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-381

Query Match      94.4%; Score 101; DB 13; Length 451;
Best Local Similarity 95.5%; Pred. No. 1.5e-08;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      428 HSQMAVHKLAKSIPLRRQVTVS 449

RESULT 13
US-10-087-192-384
; Sequence 384, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586

; Sequence 4, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-4

Query Match      94.4%; Score 101; DB 13; Length 609;
Best Local Similarity 95.5%; Pred. No. 2.1e-08;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HSQMAVHKLAKSIPLRRQVTVS 22
Db      586 HSQMAVHKLAKSIPLRRQVTES 607

RESULT 14
US-10-394-322A-27
; Sequence 27, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-27

Query Match      77.6%; Score 83; DB 15; Length 821;
Best Local Similarity 85.7%; Pred. No. 3.5e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 SQMAVHKLAKSIPLRRQVTVS 22
Db      411 SQPAVHKLTKRIPLRRQVTVS 431

RESULT 15
US-10-302-812-44
; Sequence 44, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; TITLE OF INVENTION: TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-44

Query Match      77.6%; Score 83; DB 15; Length 821;
Best Local Similarity 85.7%; Pred. No. 3.5e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 SQMAVHKLAKSIPLRRQVTVS 22
Db      411 SQPAVHKLTKRIPLRRQVTVS 431
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Db 411 SQPAVHKLTKRIPLRROTVS 431

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 14, 2005, 03:11:53 ; Search time 37.9211 Seconds
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Title: US-09-757-415a-3

Perfect score: 107

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	100.0	2360	4	US-09-023-655-1288
2	107	100.0	2469	1	US-07-997-133-2
3	107	100.0	2469	1	US-08-459-296-1
4	107	100.0	2469	5	US-07-997-133-2
5	107	100.0	2662	2	US-08-451-822A-14
6	107	100.0	2662	3	US-08-323-430-14
7	107	100.0	2733	1	US-08-371-001-14
8	107	100.0	2733	5	PCT-US96-00331-14
9	107	100.0	3503	1	US-07-631-717A-1
10	107	100.0	3503	1	US-08-166-717D-1
11	101	94.4	3944	4	US-09-949-016-1876
12	101	94.4	3944	4	US-09-949-016-1877

13	101	94.4	3944	4	US-09-949-016-1878	Sequence 1878, Ap
14	101	94.4	3944	4	US-09-949-016-1879	Sequence 1879, Ap
15	101	94.4	3944	4	US-09-949-016-1880	Sequence 1880, Ap
16	101	94.4	3944	4	US-09-949-016-1881	Sequence 1881, Ap
17	101	94.4	3944	4	US-09-949-016-1882	Sequence 1882, Ap
18	101	94.4	3944	4	US-09-949-016-1883	Sequence 1883, Ap
19	101	94.4	3944	4	US-09-949-016-1884	Sequence 1884, Ap
20	101	94.4	3944	4	US-09-949-016-1885	Sequence 1885, Ap
21	101	94.4	3944	4	US-09-949-016-1886	Sequence 1886, Ap
22	101	94.4	3944	4	US-09-949-016-1887	Sequence 1887, Ap
23	101	94.4	3944	4	US-09-949-016-1888	Sequence 1888, Ap
24	101	94.4	3944	4	US-09-949-016-1889	Sequence 1889, Ap
25	101	94.4	3944	4	US-09-949-016-1890	Sequence 1890, Ap
26	101	94.4	3944	4	US-09-949-016-1891	Sequence 1891, Ap
27	83	77.6	2676	1	US-08-471-570-5	Sequence 1892, Ap
28	83	77.6	2676	1	US-08-471-570-7	Sequence 1893, Ap
29	83	77.6	2676	1	US-08-451-822A-15	Sequence 1894, Ap
30	83	77.6	2676	1	US-08-323-430-15	Sequence 1895, Ap
31	81	75.7	2675	1	US-08-070-165F-5	Sequence 1896, Ap
32	81	75.7	2675	2	US-08-885-418-5	Sequence 1897, Ap
33	81	75.7	2681	1	US-08-070-165F-9	Sequence 1898, Ap
34	81	75.7	2681	2	US-08-885-418-9	Sequence 1899, Ap
35	77	72.0	2079	4	US-09-949-016-3171	Sequence 1900, Ap
36	77	72.0	2079	4	US-09-949-016-3172	Sequence 1901, Ap
37	77	72.0	2079	4	US-09-949-016-3173	Sequence 1902, Ap
38	77	72.0	2079	4	US-09-949-016-3174	Sequence 1903, Ap
39	77	72.0	2079	4	US-09-949-016-3175	Sequence 1904, Ap
40	77	72.0	2079	4	US-09-949-016-3176	Sequence 1905, Ap
41	77	72.0	2079	4	US-09-949-016-3177	Sequence 1906, Ap
42	77	72.0	2079	4	US-09-949-016-3178	Sequence 1907, Ap
43	77	72.0	2079	4	US-09-949-016-3179	Sequence 1908, Ap
44	77	72.0	2079	4	US-09-949-016-3180	Sequence 1909, Ap
45	77	72.0	110266	4	US-09-949-016-14913	Sequence 1910, Ap

ALIGNMENTS

RESULT 1

US-09-023-655-1288
Sequence 1288, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g31386
US-09-023-655-1288

Alignment Scores:
Pred. No.: 4.29e-10 Length: 2360
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-023-655-1288 (1-2360)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1114 CACAGCCAGATGGCTGTGCACAGCTGGCCACAGAGCATCCCTCTGCGCAGACAGGTAACA 1173

Qy 21 ValSer 22
Db 1174 GTGTCT 1179

RESULT 2
US-07-997-133-2
; Sequence 2, Application US/07997133
; Patent No. 528855
; GENERAL INFORMATION:
; APPLICANT: Bergonzoni, Laura
; APPLICANT: Mazue, Guy
; APPLICANT: Isacchi, Antonella
; APPLICANT: Roncucci, Romeo
; APPLICANT: Sarmientos, Paolo
; TITLE OF INVENTION: Extracellular Form of the Human
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/997,133
; FILING DATE: 28-DEC-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,755
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 528855man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-226-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2466
; OTHER INFORMATION:
US-08-459-296-1
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; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-997-133-2

Alignment Scores:
Pred. No.: 4.56e-10 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1225 CACAGCCAGATGGCTGTGCACAGCTGGCCACAGAGCATCCCTCTGCGCAGACAGGTAACA 1284

Qy 21 ValSer 22
Db 1285 GTGTCT 1290

RESULT 3
US-08-459-296-1
; Sequence 1, Application US/08459296
; Patent No. 5670323
; GENERAL INFORMATION:
; APPLICANT: No. 5670323a, Michael
; APPLICANT: Gonzalez, Ana-Maria
; APPLICANT: Baird, Andrew
; TITLE OF INVENTION: PROCESS FOR DETECTION OF NEOPLASTIC
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,296
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7573-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2466
; OTHER INFORMATION:
US-08-459-296-1
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Alignment Scores:

Pred. No.: 4.56e-10 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-459-296-1 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
|||||
Db 1225 CACAGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1284

Qy 21 ValSer 22

Db 1285 GTGTCT 1290

RESULT 4

US-07-997-133-2

; Sequence 2, Application US/07997133
; GENERAL INFORMATION:
; APPLICANT: Bergonzoni, Laura
; APPLICANT: Mazue, Guy
; APPLICANT: Isacchi, Antonella
; APPLICANT: Roncucci, Romeo
; APPLICANT: Sarmientos, Paolo
; TITLE OF INVENTION: Extracellular Form of the Human
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/997,133
; FILING DATE: 28-DEC-1992
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,755
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, Norman F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-226-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-07-997-133-2

Alignment Scores:

Pred. No.: 4.56e-10 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
|||||
Db 1225 CACAGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1284

Qy 21 ValSer 22

Db 1285 GTGTCT 1290

RESULT 5

US-08-451-822A-14

; Sequence 14, Application US/08451822A
; Patent No. 5863888
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,822A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,430
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,372
; FILING DATE: 21-AUG-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990

; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A0496B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

US-08-451-822A-14

Alignment Scores:

Pred. No.: 5.04e-10 Length: 2662
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-451-822A-14 (1-2662)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
|||||
Db 1312 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371

Qy 21 ValSer 22
|||||
Db 1372 GTGTCT 1377

RESULT 6
US-08-323-430-14
; Sequence 14, Application US/08323430
; Patent No. 6344546
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schllessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323.430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A0496
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 454-3817
; TELEFAX: (215) 454-3808
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-323-430-14

Alignment Scores:
Pred. No.: 5.04e-10 Length: 2662
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-323-430-14 (1-2662)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
|||||
Db 1312 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371

Qy 21 ValSer 22
|||||
Db 1372 GTGTCT 1377

RESULT 7
US-08-371-001-14
; Sequence 14, Application US/08371001
; Patent No. 5783683
; GENERAL INFORMATION:
; APPLICANT: Morrison Ph.D., Richard
; TITLE OF INVENTION: Methods and Composition for Treating
; TITLE OF INVENTION: Tumor Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 401 "B" Street, Suite 1700
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.001
; FILING DATE: January 10, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brotman, Harris F.
; REGISTRATION NUMBER: 35,461
; REFERENCE/DOCKET NUMBER: P00095US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3630
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 210..467
; OTHER INFORMATION: FGFR1 Alpha Exon
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: "IDENTITY OF
; OTHER INFORMATION: NUCLEOTIDE PROVISIONAL"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 117
; OTHER INFORMATION: "IDENTITY OF
; OTHER INFORMATION: NUCLEOTIDE PROVISIONAL"
US-08-371-001-14

Alignment Scores:
Pred. No.: 5.22e-10 Length: 2733
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-371-001-14 (1-2733)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
|||||
Db 1342 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1401

Qy 21 ValSer 22
|||||
Db 1402 GTGTCT 1407

RESULT 8
PCT-US96-00331-14
; Sequence 14, Application PC/TUS9600331
; GENERAL INFORMATION:
; APPLICANT: GENTA INCORPORATED
; TITLE OF INVENTION: METHODS AND COMPOSITION FOR
; TREATING TUMOR CELLS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00331
; FILING DATE: 10 JANUARY 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/371,001
; FILING DATE: 10 JANUARY 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 218/068-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 210..467
; OTHER INFORMATION: FGFR1 Alpha Exon
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"
; NAME/KEY: misc_feature
; LOCATION: 117
; OTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"
PCT-US96-00331-14

Alignment Scores:
Pred. No.: 5, 22e-10 Length: 2733
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-757-415A-3 (1-22) x PCT-US96-00331-14 (1-2733)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1342 CACAGCCAGATGGCTGTGCACAAAGCTGCCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 1401

Qy 21 ValSer 22
Db 1402 GTGTCT 1407
RESULT 9
US-07-631-717A-1
; Sequence 1, Application US/07631717A
; Patent No. 5270197
; GENERAL INFORMATION:
; APPLICANT: Yavon, Avner
; APPLICANT: Ornitz, David M.
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
; TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
; TITLE OF INVENTION: FACTOR RECEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/631,717A
; FILING DATE: 19901220
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00383/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3503
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-631-717A-1

Alignment Scores:
Pred. No.: 7, 27e-10 Length: 3503
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-631-717A-1 (1-3503)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1500 CATAGCCAGATGGCTGTGCACAAAGCTGCCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 1559

Qy 21 ValSer 22
Db 1560 GTGTCA 1565

RESULT 10
US-08-166-717D-1
; Sequence 1, Application US/08166717D

; Patent No. 5789182
; GENERAL INFORMATION:
; APPLICANT: Yayon, Avner
; APPLICANT: Ornitz, David M.
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
; TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
; TITLE OF INVENTION: FACTOR RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,717D
; FILING DATE: 12/14/93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/631,717
; FILING DATE: 12/20/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Kristina Bieker-Brady
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 00383/017002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-4123
; TELEFAX: (617) 723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3503
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-166-717D-1

Alignment Scores: 3503
Pred. No.: 7.27e-10 Length: 3503
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-166-717D-1 (1-3503)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1500 CATAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 1559

Qy 21 ValSer 22
Db 1560 GTGTCA 1565

RESULT 11
US-09-949-016-1876
; Sequence 1876, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1876
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1876

Alignment Scores: 3944
Pred. No.: 1.17e-08 Length: 3944
Score: 101.00 Matches: 21
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 1
Query Match: 94.39% Indels: 0
DB: 4 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-949-016-1876 (1-3944)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1953 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 2012

Qy 21 ValSer 22
Db 2013 GAAAGT 2018

RESULT 12
US-09-949-016-1877
; Sequence 1877, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1877
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1877

Alignment Scores: 3944
Pred. No.: 1.17e-08 Length: 3944
Score: 101.00 Matches: 21
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 1
Query Match: 94.39% Indels: 0
DB: 4 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-949-016-1877 (1-3944)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1953 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 2012

Qy 21 ValSer 22


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Db      2013 GAAAGT 2018
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RESULT 13
US-09-949-016-1878
; Sequence 1878, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1878
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1878

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:              4      Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1878 (1-3944)
Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
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Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
|||
Db      2013 GAAAGT 2018

RESULT 14
US-09-949-016-1879
; Sequence 1879, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1879
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1879

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
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Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:              4      Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1879 (1-3944)
Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
|||
Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
|||
Db      2013 GAAAGT 2018

RESULT 15
US-09-949-016-1880
; Sequence 1880, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1880
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1880

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:              4      Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1880 (1-3944)
Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
|||
Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
|||
Db      2013 GAAAGT 2018

Search completed: February 14, 2005, 03:23:25
Job time : 40.9211 secs
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GenCore version 5.1.6
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Run on: February 14, 2005, 03:17:13 : Search time 121.145 Seconds
(without alignment)
1071.529 Million cell updates/sec

Title: US-09-757-415A-3
Perfect score: 107
Sequence: 1 HSQAVHKLAKSIPLRRQVTVS 22

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5378673 seqs, 2950229984 residues
Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -OFMT=fastp -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-THRS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09757415 @CGN 1 1 582 @runat_07022005_160042_26863
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	2360	17	US-10-641-643-1288
2	107	100.0	2469	18	US-10-664-705-12
3	107	100.0	2469	18	US-10-384-339C-71
4	107	100.0	2470	17	US-10-307-817-5
5	107	100.0	2662	16	US-10-204-041-1
6	107	100.0	2731	17	US-10-307-817-7
7	107	100.0	2737	17	US-10-307-817-3
8	107	100.0	3328	15	US-10-101-510-299
9	107	100.0	3328	18	US-10-283-975A-98
10	107	100.0	3343	17	US-10-302-812-41
11	107	100.0	3454	13	US-10-044-090-48
12	107	100.0	3726	9	US-09-925-302-271
13	107	100.0	3726	10	US-09-925-302-271
14	107	100.0	3981	18	US-10-723-860-474
15	107	100.0	4066	15	US-10-007-926A-182
16	107	100.0	4066	17	US-10-159-563-305
17	107	100.0	4444	18	US-10-723-860-5144
18	107	100.0	4628	9	US-09-805-020-11
19	107	100.0	5438	18	US-10-723-860-5897
20	101	94.4	1726	13	US-10-087-192-380
21	101	94.4	3944	13	US-10-087-192-383
22	101	94.4	11294	10	US-09-764-891-7594
23	101	94.4	15123	10	US-09-764-891-7595
24	101	94.4	58215	13	US-10-087-192-379
25	101	94.4	75853	13	US-10-087-192-382
26	87	81.3	505	10	US-09-918-995-4697
27	84	78.5	1451	9	US-09-917-800A-1466
28	83	77.6	2466	18	US-10-384-339C-85
29	83	77.6	2650	10	US-09-954-556-28
30	83	77.6	2826	10	US-09-954-556-21
31	83	77.6	2868	10	US-09-954-556-19
32	83	77.6	2923	10	US-09-954-556-20
33	83	77.6	2941	10	US-09-954-556-18
34	83	77.6	3080	10	US-09-954-556-25
35	83	77.6	3248	17	US-10-302-812-43
36	83	77.6	3306	10	US-09-954-556-10
37	83	77.6	4268	9	US-09-954-456-293
38	83	77.6	4268	9	US-09-954-456-1599
39	83	77.6	4268	10	US-09-954-556-3
40	83	77.6	4268	11	US-09-968-007A-461
41	83	77.6	4574	18	US-10-648-593-132
42	80	74.8	99	16	US-10-199-820-78
43	77	72.0	1978	13	US-10-087-192-1130
44	77	72.0	2079	13	US-10-087-192-1133
45	77	72.0	57561	13	US-10-087-192-1129

ALIGNMENTS

RESULT 1
US-10-641-643-1288
; Sequence 1288, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1288:
SEQUENCE CHARACTERISTICS:
LENGTH: 2360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 931386
SEQUENCE DESCRIPTION: SEQ ID NO: 1288 :

US-10-641-643-1288

Alignment Scores:
Pred. No.: 2,238-09 Length: 2360
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-641-643-1288 (1-2360)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1114 CACAGCCAGATGGCTGTGCACAAAGCTGGCAAGAGCATCCCTCTCGCGACAGAGTAACA 1173
Qy 21 ValSer 22
Db 1174 GTGTCT 1179

RESULT 2
US-10-664-705-12
Sequence 12, Application US/10664705
Publication No. US20040152107A1
GENERAL INFORMATION:
APPLICANT: Altar, Anthony C.
APPLICANT: Laeng, Pascal
APPLICANT: Young, Theresa A.
APPLICANT: Charles, Vinod
APPLICANT: Bukhman, Yury
APPLICANT: Jurata, Linda
TITLE OF INVENTION: GENE SIGNATURE OF ELECTROSHOCK THERAPY AND METHODS OF USE
FILE REFERENCE: 03235/100M087-US2
CURRENT APPLICATION NUMBER: US/10/664,705
CURRENT FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: US 60/411,718
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/431,882
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/479,970
PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 2469
TYPE: DNA

ORGANISM: Rattus norvegicus
US-10-664-705-12

Alignment Scores:
Pred. No.: 2,378-09 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-664-705-12 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1225 CATAGCCAGATGGCTGTGCATTAAGCTGGTAAGAGCATCCCTCTCCGACAGAGTAACA 1284
Qy 21 ValSer 22
Db 1285 GTGTCA 1290

RESULT 3

US-10-384-339C-71
Sequence 71, Application US/10384339C
Publication No. US20040175703A1

GENERAL INFORMATION:

APPLICANT: Kreutzer, Roland

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE

FILE REFERENCE: 20200/2002

CURRENT APPLICATION NUMBER: US/10/384,339C

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: PCT/EP02/00152

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: DE 10100586.5

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: DE 10155280.7

PRIOR FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: DE 10158411.3

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: DE 10160151.4

PRIOR FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 173

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 71

LENGTH: 2469

TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

TITLE: FGPR1

PATENT DOCUMENT NUMBER: NM000604

US-10-384-339C-71

Alignment Scores:
Pred. No.: 2,378-09 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-384-339C-71 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1225 CACAGCCAGATGGCTGTGCACAAAGCTGGCAAGAGCATCCCTCTCGCGACAGAGTAACA 1284
Qy 21 ValSer 22
Db 1285 GTGTCT 1290

RESULT 4

US-10-307-817-5

Sequence 5, Application US/10307817

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; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 5
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2320)
US-10-307-817-5

Alignment Scores:
Pred. No.: 2,37e-09 Length: 2470
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-307-817-5 (1-2470)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1079 CACGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 1138
QY 21 ValSer 22
Db 1139 GTGTCT 1144

RESULT 5
US-10-204-041-1
; Sequence 1, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTANTINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 0111858.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/EP02/05420
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-041-1

Alignment Scores:
Pred. No.: 2,6e-09 Length: 2662
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-204-041-1 (1-2662)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20

; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 7
; LENGTH: 2731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2581)
US-10-307-817-7

Alignment Scores:
Pred. No.: 2,69e-09 Length: 2731
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-307-817-7 (1-2731)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1340 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 1399
QY 21 ValSer 22
Db 1400 GTGTCT 1405

RESULT 7
US-10-307-817-3
; Sequence 3, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2587)
US-10-307-817-3

Alignment Scores:
Pred. No.: 2,69e-09 Length: 2737
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

Db 1312 CACGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371
QY 21 ValSer 22
Db 1372 GTGTCT 1377

RESULT 6
US-10-307-817-7
; Sequence 7, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 7
; LENGTH: 2731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2581)
US-10-307-817-7
```

```
DB: 17 Gaps: 0
US-09-757-415A-3 (1-22) x US-10-307-817-3 (1-2737)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1346 CACAGCCAGATGGCTGTGTCACAGCTGGCCAGAGCATCCCTCTGCGCAGACAGGTAACA 1405
Qy 21 ValSer 22
Db 1406 GTGTCT 1411

RESULT 8
US-10-101-510-299
; Sequence 299, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101.510
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 299
; LENGTH: 3328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-299

Alignment Scores:
Pred. No.: 3.44e-09 Length: 3328
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-101-510-299 (1-3328)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1180 CACAGCCAGATGGCTGTGTCACAAAGCTGGCCAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
Qy 21 ValSer 22
Db 1240 GTGTCT 1245

RESULT 9
US-10-283-975A-98
; Sequence 98, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 98
; LENGTH: 3328
```

```
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-98

Alignment Scores:
Pred. No.: 3.44e-09 Length: 3328
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-283-975A-98 (1-3328)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1180 CACAGCCAGATGGCTGTGTCACAAAGCTGGCCAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
Qy 21 ValSer 22
Db 1240 GTGTCT 1245

RESULT 10
US-10-302-812-41
; Sequence 41, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; TITLE OF INVENTION: TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-812-41

Alignment Scores:
Pred. No.: 3.46e-09 Length: 3343
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-302-812-41 (1-3343)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1228 CACAGCCAGATGGCTGTGTCACAAAGCTGGCCAGAGCATCCCTCTGCGCAGACAGGTAACA 1287
Qy 21 ValSer 22
Db 1288 GTGTCT 1293

RESULT 11
US-10-044-090-48
; Sequence 48, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 3454
```

;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. US20020137081A1 493848CB1
;; NAME/KEY: unsure
;; LOCATION: 2, 9, 16, 39, 42, 68, 143, 268
;; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-48

Alignment Scores:
Pred. No.: 3.61e-09 Length: 3454
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-044-090-48 (1-3454)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1078 CACAGCCAGATGGCTGTGCAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1137

Qy 21 ValSer 22
Db 1138 GTGTCT 1143

RESULT 12

US-09-925-302-271
; Sequence 271, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 3726

;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc feature
;; LOCATION: (2586)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3523)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3664)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3687)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-271

Alignment Scores:
Pred. No.: 3.97e-09 Length: 3726
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-925-302-271 (1-3726)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1051 CACAGCCAGATGGCTGTGCAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1110
Qy 21 ValSer 22
Db 1111 GTGTCT 1116

RESULT 13

US-09-925-302-271
; Sequence 271, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 3726

;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc feature
;; LOCATION: (2586)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3523)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3664)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: misc feature
;; LOCATION: (3687)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-271

Alignment Scores:
Pred. No.: 3.97e-09 Length: 3726
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-925-302-271 (1-3726)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1051 CACAGCCAGATGGCTGTGCAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1110
Qy 21 ValSer 22
Db 1111 GTGTCT 1116

RESULT 14

US-10-723-860-474
; Sequence 474, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860

```
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 474
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-474
```

Qy 21 ValSer 22
|||||
Db 2011 GTGTCT 2016

Search completed: February 14, 2005, 05:18:15
Job time : 138.145 secs

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Alignment Scores:
Pred. No.: 4,31e-09 Length: 3981
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-723-860-474 (1-3981)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1951 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010

Qy 21 ValSer 22
Db 2011 GTGTCT 2016
```

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RESULT 15
US-10-007-926A-182
; Sequence 182, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 182
; LENGTH: 4066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: fibroblast growth factor receptor 1
; OTHER INFORMATION: (fms-related tyrosine kinase 2, pfeiffer syndrome)
; OTHER INFORMATION: (FGFR1) gene.
US-10-007-926A-182
```

```
Alignment Scores:
Pred. No.: 4,43e-09 Length: 4066
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-007-926A-182 (1-4066)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1951 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010
```